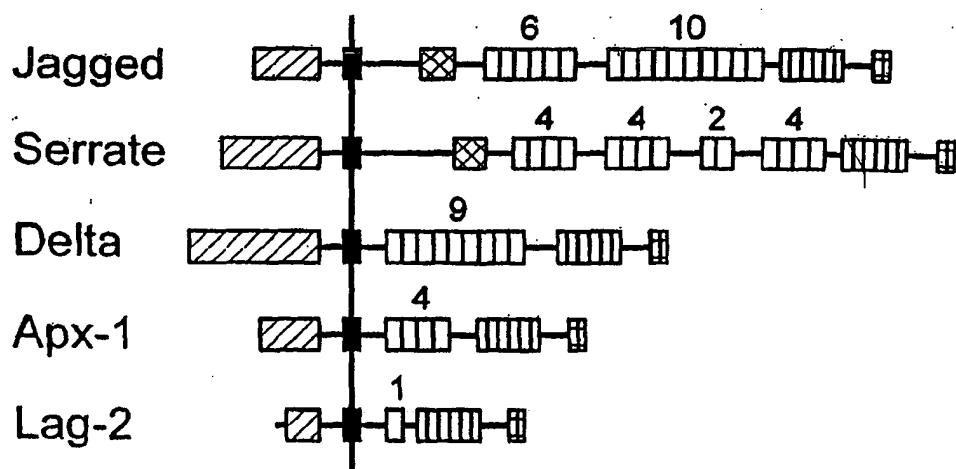


FIG. 1

Domain Structure of the Notch Ligand Family



- [diagonal lines] Intracellular Domain
- [solid black square] Transmembrane Domain
- [cross-hatch] Cys-Rich Domain
- [vertical lines] EGF Repeat Domain
- [horizontal lines] Delta Serrate Lag-2 (DSL) Domain
- [diagonal lines] Signal Peptide Domain

FIG. 2

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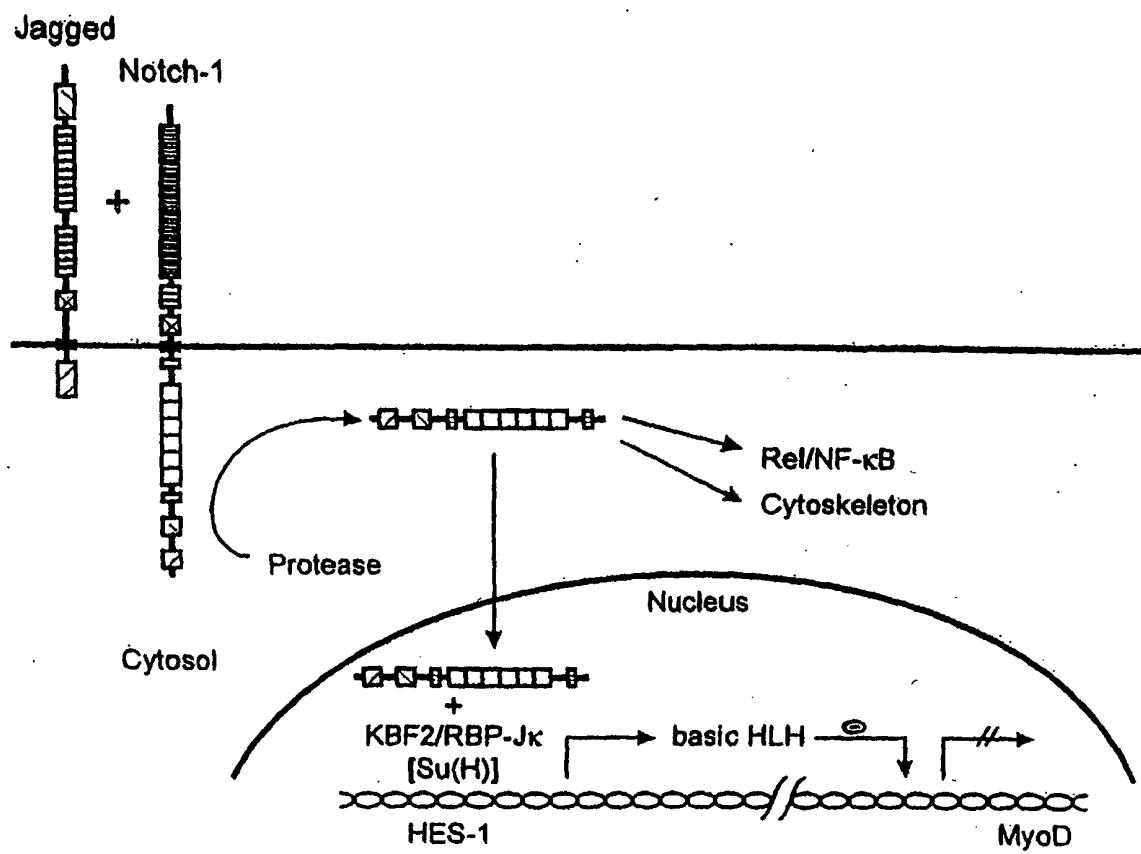


FIG. 3

Domain Structure of the Notch Receptor Family

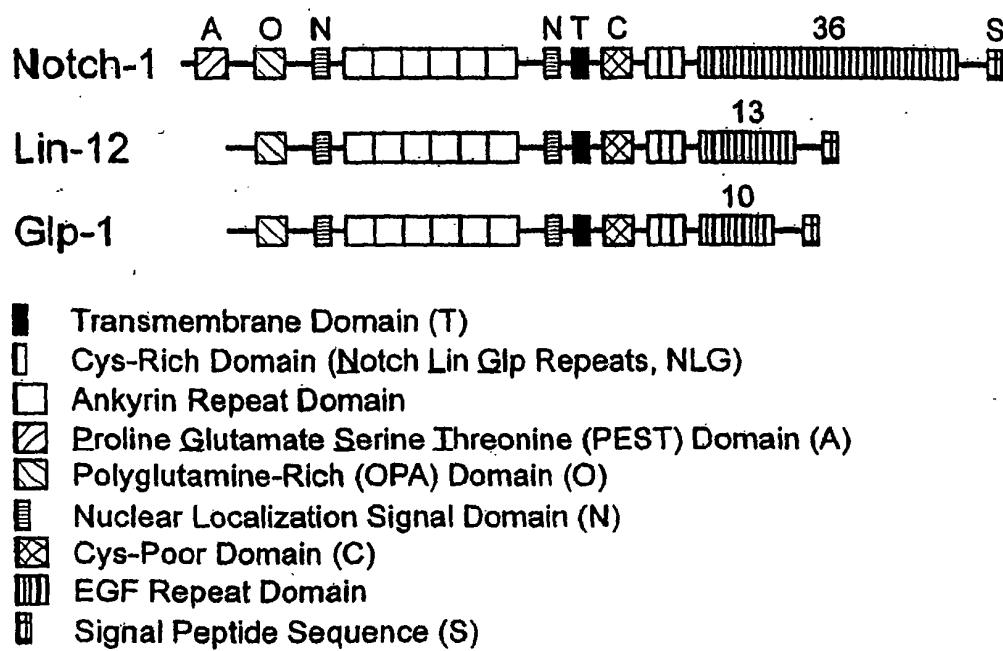


FIG.4

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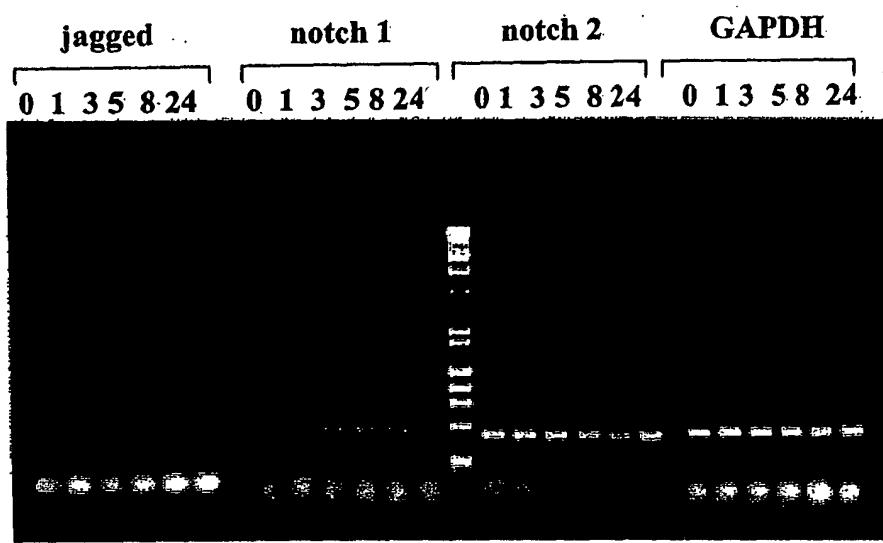


FIG. 5

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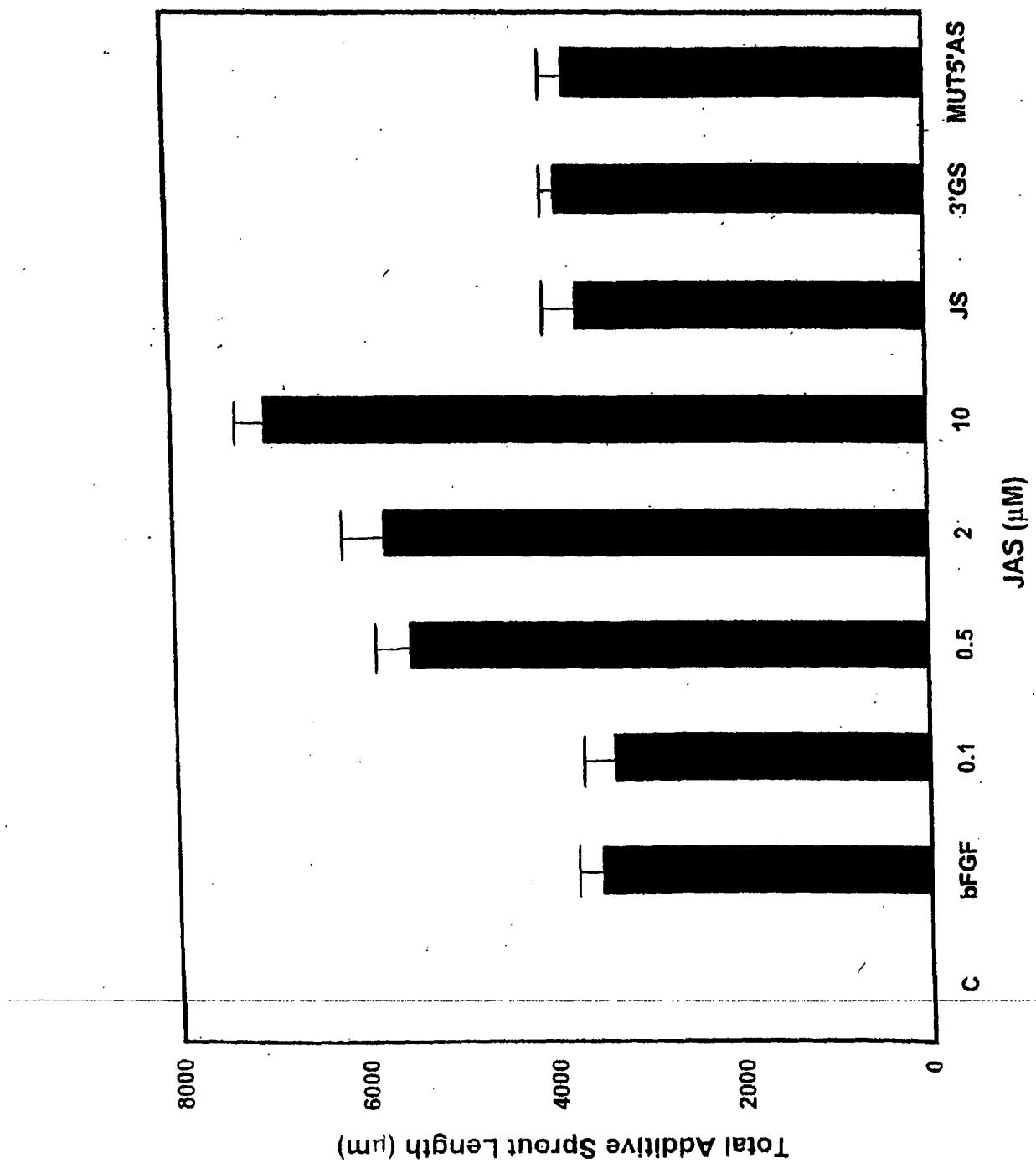


FIG. 6

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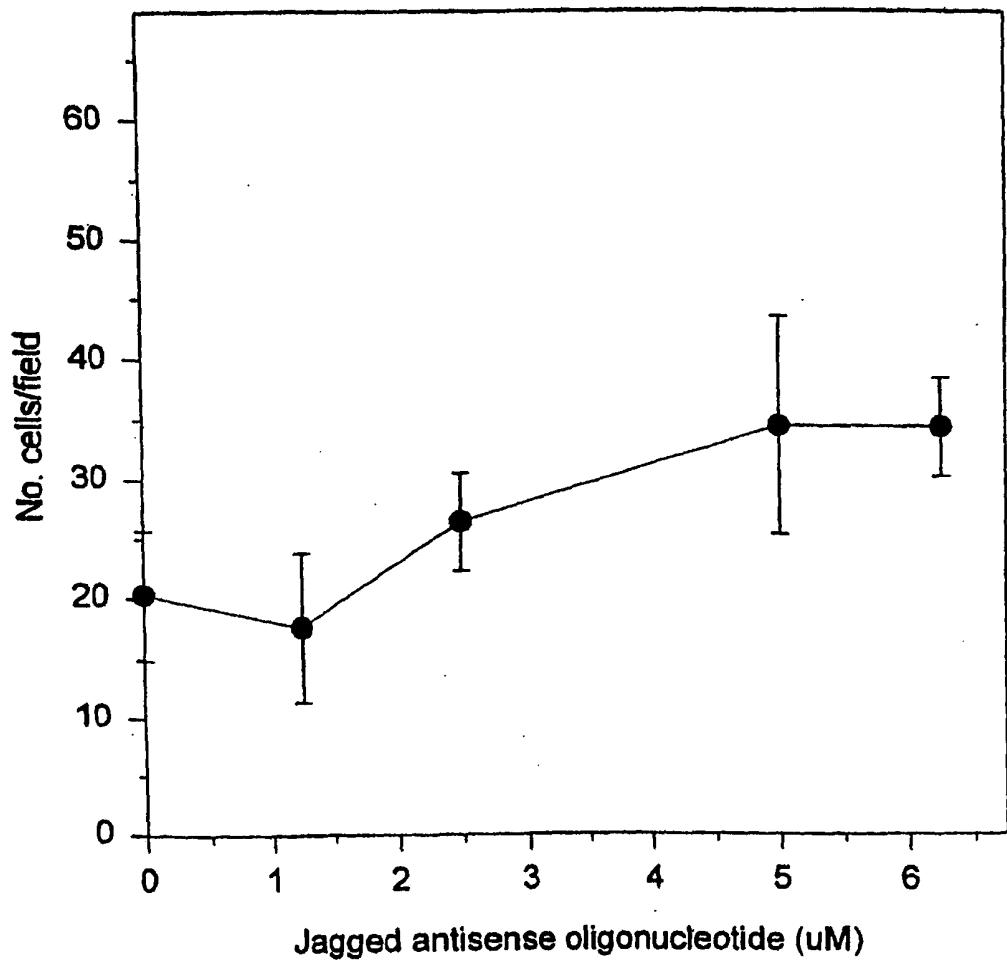


FIG. 7A

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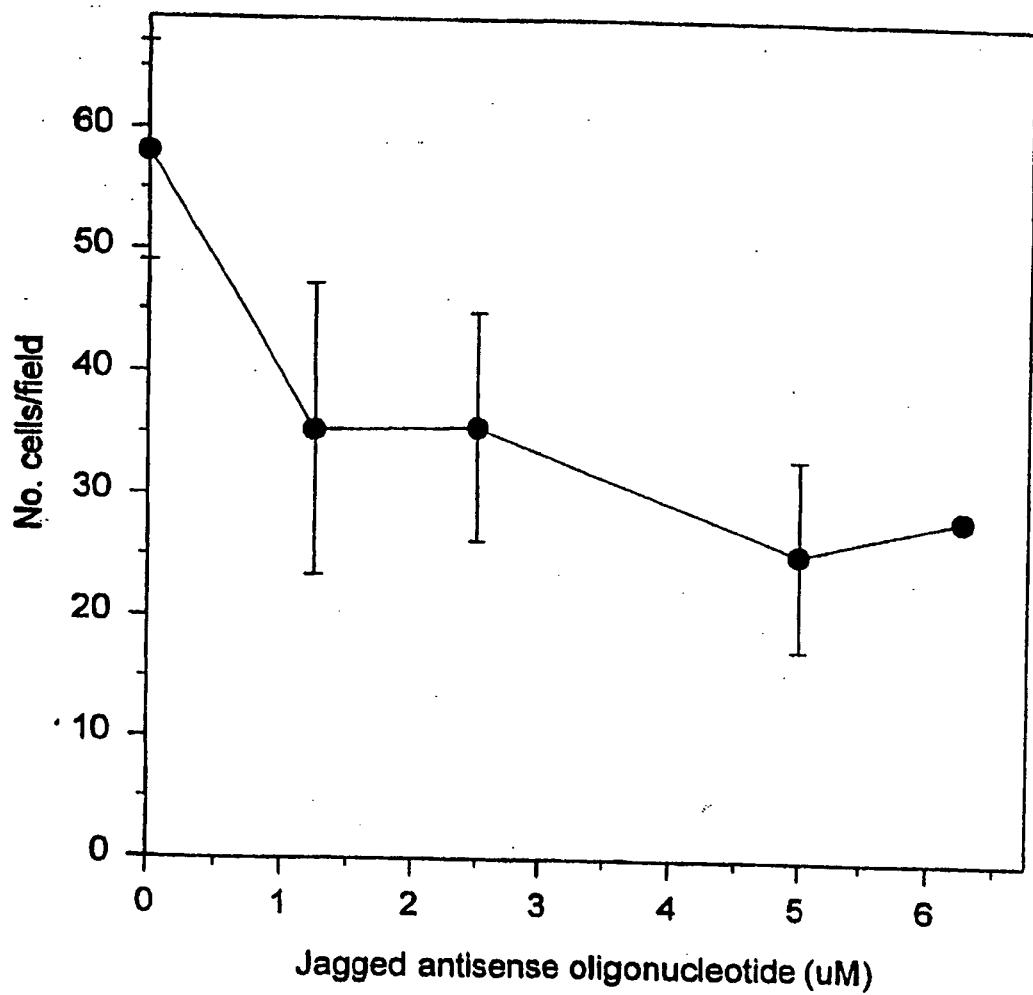


FIG. 7B

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1	MRSPRTRGRS	GRPLSLLLL	LCALRAKVCG	ASQFELEIL	SMQNVNNGELQ
51	NGNCGGARN	PGDRKCTRDE	CDTYFKVCLK	EYQSRVTAGG	PCSFSGSGSTP
101	VIGGNTFNLK	ASRGNDRNRI	VLPPSFAWPR	SYTLLVEAWD	SSNDTVQPDS
151	I TEKASHSGM	INPSRQWQTL	KQNTGVAHFE	YQIRVTCDYY	YYGFGCNKFC
201	RPRDDFFGHY	ACDQNGNKTG	MEGWMGPECN	RAICRQGCSP	KHGSCKLPGD
251	CRCQYGWQGL	YCDKCIHPG	CVHGCNEPW	QCLCETNWGG	QLCDKDLNYC
301	GTHQPCLNNG	TCSNTGPDKY	QCSCPEGYSG	PNCEIAEHAC	LSDPCHNRGS
351	CKETSLGFEC	ECPGWTGPT	CSTNIDDCSP	NNCSHGGTCQ	DLVNGFKCVC
401	PPQWTGKTCQ	LDAНЕCEAKP	CVNAKSKNL	IASYYCDCLP	GWMGQNCDIN
451	INDCLGQCQN	DASCRDLVNG	YRCICPPGYA	GDHCERDIDE	CASNPCLNNG
501	HCQNEINRFQ	CLCPGTGFSGN	LCQLDIDYCE	PNPCQNGAQC	YNRASDYFCK
551	CPEDYEGKNC	SHLKDHCRTT	PCEVIDSCTV	AMASNDTPEG	VRYISSNVCG
601	PHGKCKSQSG	GKFTCDCNKG	FTGTYCHENI	NDCESNPCRN	GGTCIDGVNS
651	YKCICSDGWE	GAYCETNIND	CSQNPCHNGG	TCRDLVNDFY	CDCKNGWKKG
701	TCHSRDSQCD	EATCNNGGT	YDEGDAFKCM	CPGGWEGTT	NIARNSSCLP
751	NPCHNGGTCV	VNGESFTCVC	KEGWEGPICA	QNTNDCSPHP	CYNSGTCVDG
801	DNWYRCECAP	GFAGPDCRIN	INECQSSPCA	FGATCVDEIN	GYRCVCPPGH
851	SGAKCQEVS	RPCITMGSVI	PDGAKWDDDC	NTCQCLNGRI	ACSKVWCGR
901	PCLLHKGHSE	CPSGQSCIPI	LDDQCFVHPC	TGVGECRSSS	LQPVTKCTS
951	DSYYQDN CAN	ITFTFNKEMM	SPGLTTEHIC	SELRLNLILK	NVSAEYSIYI
1001	ACEPSPSANN	EIHVAISAED	IRDDGNPIKE	ITDKIIDLVS	KRDGNSSLIA
1051	AVAEVRVQRR	PLKNRTDFLV	PLLSSVLTVA	WICCLVTAFY	WCLRKRRKPG
1101	SHTHSASEDN	TTNNVREQLN	QIKNPIEKHG	ANTVPIKDYE	NKNSKMSKIR
1151	THNSEVEEDD	MDKHQQKARF	GKQPAYTLVD	REEKPPNGTP	TKHPNWTNKQ
1201	DNRDLESAQS	LNRMEYIV			

FIG. 8A

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1	ATGCGTTCCC	CACGGACRCG	CGGCCGGTCC	GGGCGCCCCC	TAAGCCTCCT
51	GCTCGCCCTG	CTCTGTGCC	TGCGAGCAA	GGTGTGTGGG	GCCTCGGGTC
101	AGTTCGAGTT	GGAGATCCTG	TCCATGCAGA	ACGTGAACGG	GGAGCTGCAG
151	AACGGGAACT	GCTGGGGCGG	CGCCCGGAAC	CCGGGAGACC	GCAAGTGCAC
201	CCGCGACGAG	TGTGACACAT	ACTTCAAAGT	GTGCCTCAAG	GAGTATCAGT
251	CCCGCGTCAC	GGCCGGGGGG	CCCTGCAGCT	TCGGCTCAGG	GTCCACGCCT
301	GTCATCGGGG	GCAACACCTT	CAACCTCAAG	GCCAGCCGCG	GCAACGACCG
351	CAACCGCATC	GTGCTGCC	TCAGTTCGC	CTGGCCGAGG	TCCTATACGT
401	TGCTTGTGGA	GGCGTGGGAT	TCCAGTAATG	ACACCGTTCA	ACCTGACAGT
451	ATTATTGAAA	AGGCTTCTCA	CTCGGGCATG	ATCAACCCCA	GCCGGCAGTG
501	GCAGACGCTG	AAGCAGAAC	CGGGCGTTGC	CCACTTTGAG	TATCAGATCC
551	GCGTGACCTG	TGATGACTAC	TAATATGGCT	TTGGCTGYAA	TAAGTTCTGC
601	CGCCCCAGAG	ATGACTTCTT	TGGACACTAT	GCCTGTGACC	AGAATGGCAA
651	CAAAACTTGC	ATGGAAGGCT	GGATGGGCC	CGAATGTAAC	AGAGCTATTT
701	GCCGACAAGG	CTGCAGTCCT	AAGCATGGGT	CTTGCAAAC	CCCAGGTGAC
751	TGCAGGTGCC	AGTAYGGCTG	GCAAGGCCTG	TACTGTGATA	AGTGCATCCC
801	ACACCCGGGA	TGCGTCCACG	GCATCTGTAA	TGAGCCCTGG	CAGTGCCTCT
851	GTGAGACCAA	CTGGGGCGGC	CAGCTCTGTG	ACAAAGATCT	CAATTACTGT
901	GGGACTCATC	AGCCGTGTCT	CAACGGGGGA	ACTTGTAGCA	ACACAGGCC
951	TGACAAATAT	CAGTGTTC	GCCCTGAGGG	GTATTCAAGGA	CCCAACTGTG
1001	AAATTGCTGA	GCACGCC	CTCTCTGATC	CCTGTACAA	CAGAGGCAGC
1051	TGTAAGGAGA	CCTCCCTGGG	CTTGAGTGT	GAGTGTCCC	CAGGCTGGAC
1101	CGGCCCCACA	TGCTCTACAA	ACATTGATGA	CTGTTCTCCT	AATAACTGTT
1151	CCCACGGGG	CACCTGCCAG	GACCTGGTTA	ACGGATTAA	GTGTGTGTG
1201	CCCCCACAGT	GGACTGGAA	AACGTGCCAG	TTAGATGCAA	ATGAATGTGA
1251	GGCCAAACCT	TGTGTAAACG	CCAAATCCTG	TAAGAATCTC	ATTGCCAGCT
1301	ACTACTGCGA	CTGTCTTCCC	GGCTGGATGG	GTCAGAATTG	TGACATAAAT
1351	ATTAATGACT	GCCTTGGCCA	GTGTCAGAAT	GACGCCCTC	GTCGGGATT
1401	GGTTAATGGT	TATCGCTGTA	TCTGTCCACC	TGGCTATGCA	GGCGATCACT
1451	GTGAGAGAGA	CATCGATGAA	TGTGCCAGCA	ACCCCTGTT	GAATGGGGT
1501	CACTGTAGA	ATGAAATCAA	CAGATTCCAG	TGTCTGTGTC	CCACTGGTTT
1551	CTCTGGAAAC	CTCTGTCA	TGGACATCGA	TTATTGTGAG	CCTAATCCCT
1601	GCCAGAACGG	TGCCAGTGC	TACAACCGTG	CCAGTGACTA	TTTCTGCAAG
1651	TGCCCCGAGG	ACTATGAGGG	CAAGAACTGC	TCACACCTGA	AAGACCACTG
1701	CCGCACGACC	CCCTGTGAAG	TGATTGACAG	CTGCACAGTG	GCCATGGCTT
1751	CCAACGACAC	ACCTGAAGGG	GTGCGGTATA	TTTCCTCCAA	CGTCTGTGGT
1801	CCTCACGGGA	AGTGAAGAG	TCAGTCGGGA	GGCAAATTCA	CCTGTGACTG
1851	TAACAAAGGC	TTCACGGGA	CATACTGCCA	TGAAAATATT	AATGACTGTG
1901	AGAGCAACCC	TTGTAGAAC	GGTGGCACTT	GCATCGATGG	TGTCAACTCC
1951	TACAAGTGCA	TCTGTAGTGA	CGGCTGGGAG	GGGGCCTACT	GTGAAACCAA
2001	TATTAATGAC	TGCAGGCCAGA	ACCCCTGCCA	CAATGGGGC	ACGTGTCGCG

FIG. 8B

2051 ACCTGGTCAA TGACTTCTAC TGTGACTGTA AAAATGGGTG GAAAGGAAAG
 2101 ACCTGCCACT CACCGTACAG TCAGTGTGAT GAGGCCACGT GCAACAAACGG
 2151 TGGCACCTGC TATGATGAGG GGGATGCTTT TAAGTCATG TGTCCCTGGCG
 2201 GCTGGGAAGG AACAAACCTGT AACATAGCCC GAAACAGTAG CTGCCTGCC
 2251 AACCCCTGCC ATAATGGGGG CACATGTGTG GTCAACGGCG AGTCCTTTAC
 2301 GTGCGTCTGC AAGGAAGGCT GGGAGGGGCC CATCTGTGCT CAGAATACCA
 2351 ATGACTGCCAG CCCTCATCCC TGTTACAACA CGGGCACCTG TGTGGATGGA
 2401 GACAACCTGGT ACCGGTGCAG ATGTGCCCG GGTGTTGCTG GGCCCCGACTG
 2451 CAGAATAAAC ATCAATGAAT GCCAGTCTTC ACCTTGTCGCTC TTTGGAGCGA
 2501 CCTGTGTGGA TGAGATCAAT GGCTACCGGT GTGTCGCCC TCCAGGGCAC
 2551 AGTGGTGCCA AGTGCCAGGA AGTTCAAGGG AGACCTTGCA TCACCATTGGG
 2601 GAGTGTGATA CCAGATGGGG CCAAATGGGA TGATGACTGT AATACCTGCC
 2651 AGTGCCTGAA TGGACGGATC GCCTGCTCAA AGGTCTGGTG TGGCCCTCGA
 2701 CCTTGCCTGC TCCACAAAGG GCACAGCGAG TGCCCCAGCG GGCAGAGCTG
 2751 CATCCCCATC CTGGACGACCC AGTGCCTCGT CCACCCCTGC ACTGGTGTGG
 2801 GCGAGTGTGCG GTCTTCCAGT CTCCAGCCGG TGAAGACAAA GTGCACCTCT
 2851 GACTCCTATT ACCAGGATAA CTGTGCGAAC ATCACATTAA CCTTTAACAA
 2901 GGAGATGATG TCACCAGGTC TTACTACGGA GCACATTGCA AGTGAATTGA
 2951 GGAATTGAA TATTTGAAAG AATGTTCCG CTGAATATTC AATCTACATC
 3001 GCTTGCAGGC CTTCCCCCTTC AGCGAACAAAT GAAATACATG TGGCCATTTC
 3051 TGCTGAAGAT ATACGGGATG ATGGGAACCC GATCAAGGAA ATCACTGACA
 3101 AAATAATCGA TCTTGTAGT AAACGTGATG GAAACAGCTC GCTGATTGCT
 3151 GCCGTTGCAG AAGTAAGAGT TCAGAGGCGG CCTCTGAAGA ACAGAACAGA
 3201 TTTCCTTGTG CTCCTGCTGA GCTCTGTCTT AACTGTGGCT TGGATCTGTT
 3251 GCTTGGTGAC GGCCTTCTAC TGTTGCCTGC GGAAGCGGCG GAAGCCGGC
 3301 AGCCACACAC ACTCAGCCTC TGAGGACAAC ACCACCAACA ACGTGCAGGA
 3351 GCAGCTGAAC CAGATAAAAA ACCCCATTGA GAAAATGGG GCCAACACGG
 3401 TCCCCATCAA GGATTACGAG AACAAAGAACT CAAAATGTC TAAAATAAGG
 3451 ACACACAATT CTGAAGTAGA AGAGGACGAC ATGGACAAAC ACCAGCAGAA
 3501 AGCCCCGGTT GGCAAGCAGC CGGGCTATAC GCTGGTAGAC AGAGAAGAGA
 3551 AGCCCCCCAA CGGCACGCCG ACAAAACACC CAAACTGGAC AAACAAACAG
 3601 GACAACAGAG ACTTGGAAAG TGCCCCAGAGC TTAAACCGAA TGGAGTACAT
 3651 CGTATAG

FIG. 8C

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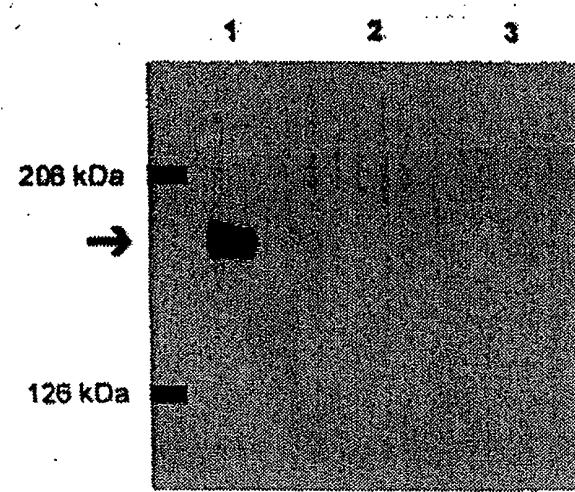


FIG. 9

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FIG. 10A

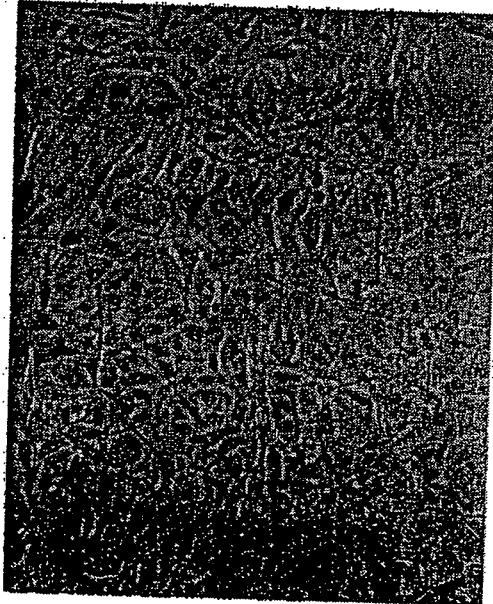


FIG. 10C

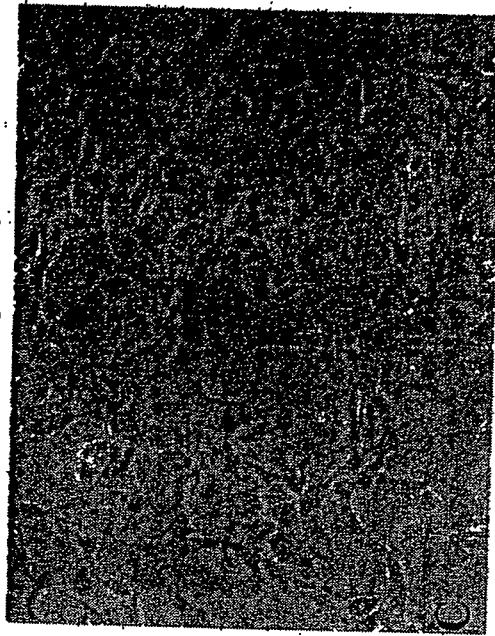


FIG. 10B

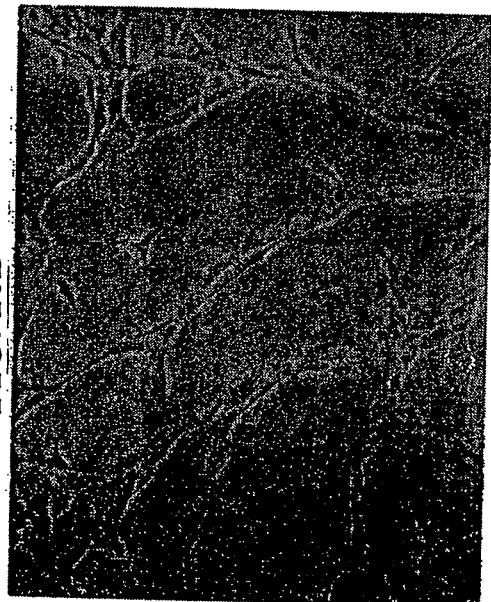
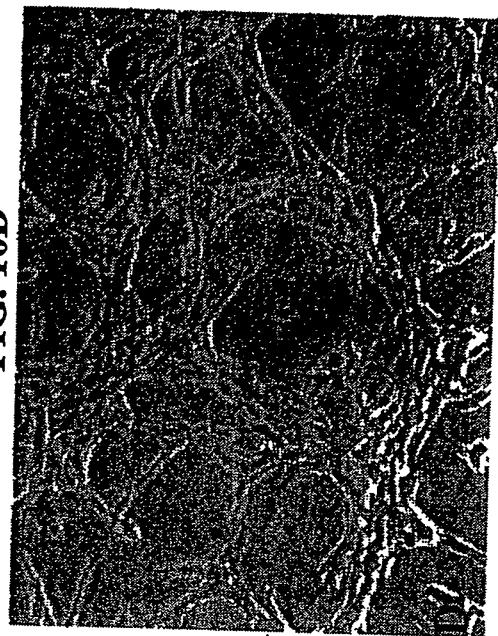


FIG. 10D



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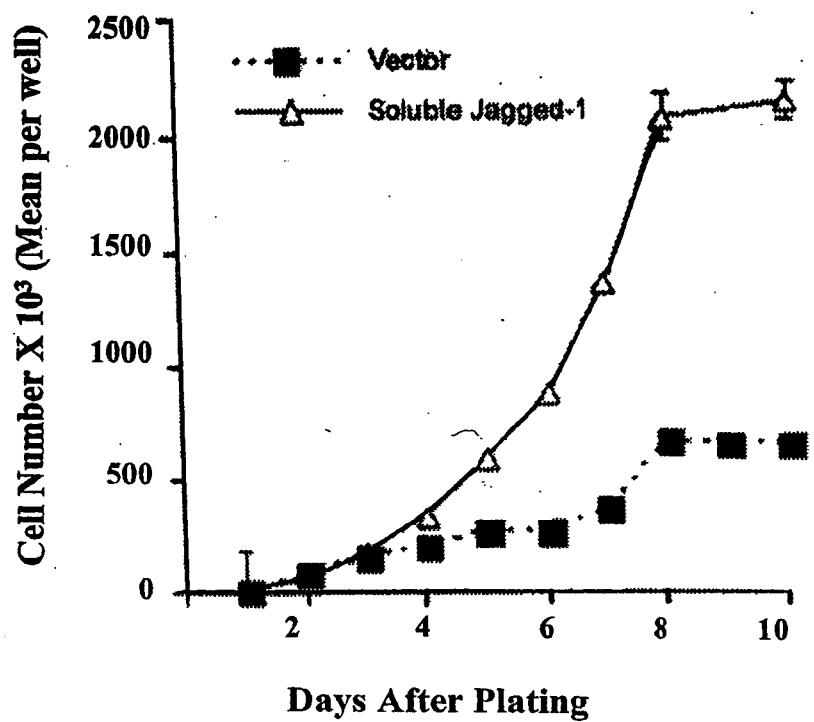


FIG. 11

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FIG. 12A

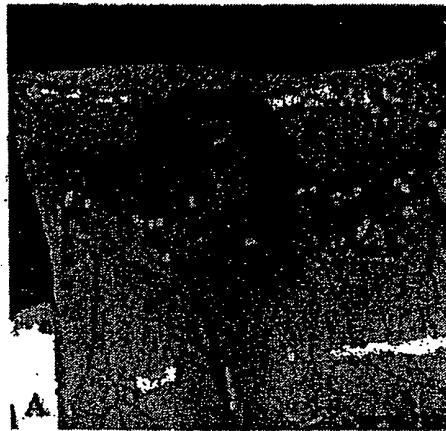


FIG. 12B



FIG. 12C

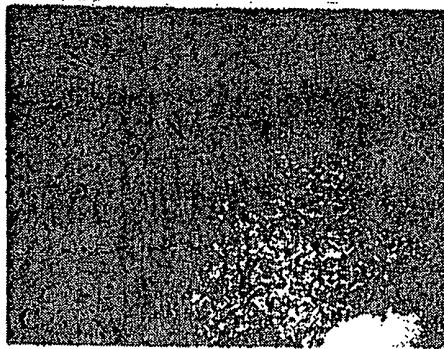
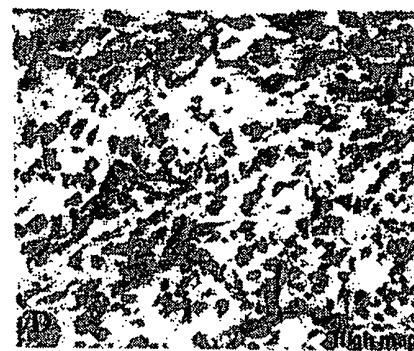


FIG. 12D



1 MRSPRTRGRS RPLSLLLALL CALRAKVCGA SGQFELEILS MQNVNGELQN
51 GNCCGGARNP GDRKCTRDEC DTYFKVCLKE YQSRVTAGGP CSFGSGSTPV
101 IGGNTFNLKA SRGNDRNRIV LPPFSFAWPRS YTLLVEAWDS SNDTVQPDSI
151 IEKASHSGMI NPSRQWQTLK QNTGVAHFEY QIRVTCDYYY YGFGCNKFCR
201 PRDDFFGHYA CDQNGNKTCM EGWMGPECNR AICRQGCSPK HGSCKLPGDC
251 RCQYGWQGLY CDKCIPHPGC VHGISNEPWQ CLCETNWGGQ LCDKDLNYCG
301 THQPCLNNGGT CSNTGPDKYQ CSCPEGYSGP NCEIAEHACL SDPCHNRGSC
351 KETSLGFECE CSPGWTGPTC STNIDDCSPN NCSHGGTCQD LVNGFKCVCP
401 PQWTGKTCQL DANECEAKPC VNAKSKNLI ASYYCDCLPG WMGQNCINI
451 NDCLGQCQND ASCRDLVNGY RCICPPGYAG DHCRDIDEA ASNPLNNGH
501 CQNEINRFQC LCPTGFSGNL CQLDIDYCEP NPCQNGAQCY NRASDYFCKC
551 PEDYEGKNCS HLKDHCRTTP CEVIDSCTVA MASNDTPEGV RYISSNVCGP
601 HGKCKSQSGG KFTCDCNKGF TGTYCHENIN DCESNPCCRNG GTCIDGVNSY
651 CICSDGWEGA YCETNINDCS QNPCHNGGTC RDLVNDFYCD CKNGWKGKTC
701 HSRDSQCDEA TCNNGGTCYD EGDAFKCMCP GGWEGETTCNI ARNSSCLPNP
751 CHNGGTCVNN GESFTCVCXE GWEGPICAQN TNDCSPHPCY NSGTCVDGDN
801 WYRCECAPGF AGPDCRININ ECQSSPCAFG ATCVDEINGY RCVCPPGHSG
851 AKCQEVSgrp CITMGSVIPD GAKWDDDCTN CQCLNGRIAC SKVWCGRPC
901 LLHKGHSECP SGQSCIPILD DQCFVHPCTG VGECRSSLQ PVTKCTSDS
951 YYQDNCANIT FTFNKEMMSP GLTTEHICSE LRNLNILKNV SAEYSIYIAC
1001 EPSPSANNEI HVAISAEDIR DDGNPIKEIT DKIIDLVSKR DGNSSLIAAV
1051 AEVRVQRRPL KNRTD

FIG. 13A

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1	ATGCGTTCCC	CACGGACRCG	CGGCCGGTCC	GGGCGCCCCC	TAAGCCTCCT
51	GCTCGCCCTG	CTCTGTGCC	TGCGAGCCAA	GGTGTGTGGG	GCCTCGGGTC
101	AGTCGAGTT	GGAGATCCTG	TCCATGCAGA	ACGTGAACGG	GGAGCTGCAG
151	AACGGGAACT	GCTGCGGCAG	CGCCCGGAAC	CGGGGAGACC	GCAAGTGCAC
201	CCCGGACGAG	TGTGACACAT	ACTTCAAAGT	GTGCCTCAAG	GAGTATCAGT
251	CCCGCGTCAC	GGCCGGGGGG	CCCTGCAGCT	TCGGCTCAGG	GTCCACGCCT
301	GTCATCGGGG	GCAACACCTT	CAACCTCAAG	GCCAGCCGCG	GCAACGACCG
351	CAACCGCATC	GTGCTGCCTT	TCAGTTTCGC	CTGGCCGAGG	TCCTATACTG
401	TGCTTGTGGA	GGCGTGGGAT	TCCAGTAATG	ACACCGTTCA	ACCTGACAGT
451	ATTATTGAAA	AGGCTTCTCA	CTCGGGCATG	ATCAACCCCC	GCCGGCAGTG
501	GCAGACGCTG	AAGCAGAAC	CGGGCGTTGC	CCACTTTGAG	TATCAGATCC
551	GCGTGACCTG	TGATGACTAC	TACTATGGCT	TTGGCTGYAA	TAAGTTCTGC
601	CGCCCCAGAG	ATGACTTCTT	TGGACACTAT	GCCTGTGACC	AGAATGGCAA
651	AAAAACTTGC	ATGGAAGGCT	GGATGGGCC	CGAATGTAAC	AGAGCTATTT
701	GCCGACAAAGG	CTGCAGTCCT	AAGCATGGGT	CTTGCAAACT	CCCAGGTGAC
751	TGCAGGTGCC	AGTAYGGCTG	GCAAGGCCTG	TACTGTGATA	AGTGCATCCC
801	ACACCCGGGA	TGCGTCCACG	GCATCTGTAA	TGAGCCCTGG	CAGTGCCTCT
851	GTGAGACCAA	CTGGGGCGGC	CAGCTCTGTG	ACAAAGATCT	CAATTACTGT
901	GGGACTCATC	AGCCGTGTCT	CAACGGGGGA	ACTTGTAGCA	ACACAGGCC
951	TGACAAATAT	CAGTGTTCCT	GCCCTGAGGG	GTATTCAAGGA	CCCAACTGTG
1001	AAATTGCTGA	GCACGCCCTGC	CTCTCTGATC	CCTGTCACAA	CAGAGGCAGC
1051	TGTAAGGAGA	CCTCCCTGGG	CTTGAGTGT	GAGTGTCCC	CAGGCTGGAC
1101	CGGCCCCACA	TGCTCTACAA	ACATTGATGA	CTGTTCTCCT	AATAACTGTT
1151	CCCACGGGGG	CACCTGCCAG	GACCTGGTTA	ACGGATTAA	GTGTGTGTGC
1201	CCCCCACAGT	GGACTGGGAA	AACGTGCCAG	TTAGATGCAA	ATGAATGTGA
1251	GGCCAAACCT	TGTGTAAACG	CCAAATCCTG	TAAGAATCTC	ATTGCCAGCT
1301	ACTACTGCGA	CTGTCTTCCC	GGCTGGATGG	GTCAGAATTG	TGACATAAAT
1351	ATTAATGACT	GCCTTGGCCA	GTGTCAGAAT	GACGCCCTCCT	GTCGGGATTT
1401	GGTTAATGGT	TATCGCTGTA	TCTGTCCACC	TGGCTATGCA	GGCGATCACT
1451	GTGAGAGAGA	CATCGATGAA	TGTGCCAGCA	ACCCCTGTTT	GAATGGGGGT

FIG. 13B

1501	CACTGTCAGA	ATGAAATCAA	CAGATTCCAG	TGTCTGTGTC	CCACTGGTTT
1551	CTCTGGAAAC	CTCTGTCAGC	TGGACATCGA	TTATTGTGAG	CCTAATCCCT
1601	GCCAGAACGG	TGCCCGAGTG	TACAACCCTG	CCAGTGACTA	TTTCTGCAAG
1651	TGCCCGAGG	ACTATGAGGG	CAAGAACTGC	TCACACCTGA	AAGACCACTG
1701	CCGCACGACC	CCCTGTGAAG	TGATTGACAG	CTGCACAGTG	GCCATGGCTT
1751	CCAACGACAC	ACCTGAAGGG	GTGCGGTATA	TTTCCTCCAA	CGTCTGTGGT
1801	CCTCACGGGA	AGTGCAAGAG	TCAGTCGGGA	GGCAAATTCA	CCTGTGACTG
1851	TAACAAAGGC	TTCACGGGAA	CATACTGCCA	TGAAAATATT	AATGACTGTG
1901	AGAGCAACCC	TTGTAGAAAC	GGTGGCACTT	GCATCGATGG	TGTCAACTCC
1951	TACAAGTGCA	TCTGTAGTGA	CGGCTGGGAG	GGGGCCTACT	GTGAAACCAA
2001	TATTAATGAC	TGCAGCCAGA	ACCCCTGCCA	CAATGGGGC	ACGTGTCGCG
2051	ACCTGGTCAA	TGACTTCTAC	TGTGACTGTA	AAAATGGGTG	GAAAGGAAAG
2101	ACCTGCCACT	CACGTGACAG	TCAGTGTGAT	GAGGCCACGT	GCAACAAACGG
2151	TGGCACCTGC	TATGATGAGG	GGGATGCTTT	TAAGTGCATG	TGTCCCTGGCG
2201	GCTGGGAAGG	AACAACCTGT	AACATAGCCC	GAAACAGTAG	CTGCCTGCC
2251	AACCCCTGCC	ATAATGGGGG	CACATGTGTG	GTCAACGGCG	AGTCCTTTAC
2301	GTGCGTCTGC	AAGGAAGGCT	GGGAGGGGCC	CATCTGTGCT	CAGAATAACCA
2351	ATGACTGCAG	CCCTCATCCC	TGTTACAACA	GCAGCACCTG	TGTGGATGGA
2401	GACAACCTGGT	ACCGGTGCGA	ATGTGCCCG	GGTTTGCTG	GGCCCGACTG
2451	CAGAATAAAC	ATCAATGAAT	GCCAGTCTTC	ACCTTGTGCC	TTTGGAGCGA
2501	CCTGTGTGGA	TGAGATCAAT	GGCTACCGGT	GTGTCTGCC	TCCAGGGCAC
2551	AGTGGTGCCA	AGTGCCAGGA	AGTTTCAGGG	AGACCTTGCA	TCACCATGGG
2601	GAGTGTGATA	CCAGATGGGG	CCAAATGGGA	TGATGACTGT	AATACCTGCC
2651	AGTGCCTGAA	TGGACGGATC	GCCTGCTCAA	AGGTCTGGTG	TGGCCCTCGA
2701	CCTGCCTGC	TCCACAAAGG	GCACAGCGAG	TGCCCCAGCG	GGCAGAGCTG
2751	CATCCCCATC	CTGGACGACC	AGTGCCTCGT	CCACCCCTGC	ACTGGTGTGG
2801	GCGAGTGTG	GTCTTCCAGT	CTCCAGCCGG	TGAAGACAAA	GTGCACCTCT
2851	GAECTCCTATT	ACCAGGATAA	CTGTGCGAAC	ATCACATTTA	CCTTTAACAA
2901	GGAGATGATG	TCACCAGGTC	TTACTACGGA	GCACATTGCA	AGTGAATTGA
2951	GGAATTGAA	TATTTGAAG	AATGTTCCG	CTGAATATTG	AATCTACATC
3001	GCTTGCAGC	CTTCCCCCTTC	AGCGAACAAAT	GAAATACATG	TGGCCATTTC
3051	TGCTGAAGAT	ATACGGGATC	ATGGGAACCC	GATCAAGGAA	ATCACTGACA
3101	AAATAATCGA	TCTTGTAGT	AAACGTGATG	GAAACAGCTC	GCTGATTGCT
3151	GCCGTTGCAG	AAGTAAGAGT	TCAGAGGCCG	CCTCTGAAGA	ACAGAACAGA
3201	T				

FIG. 13C